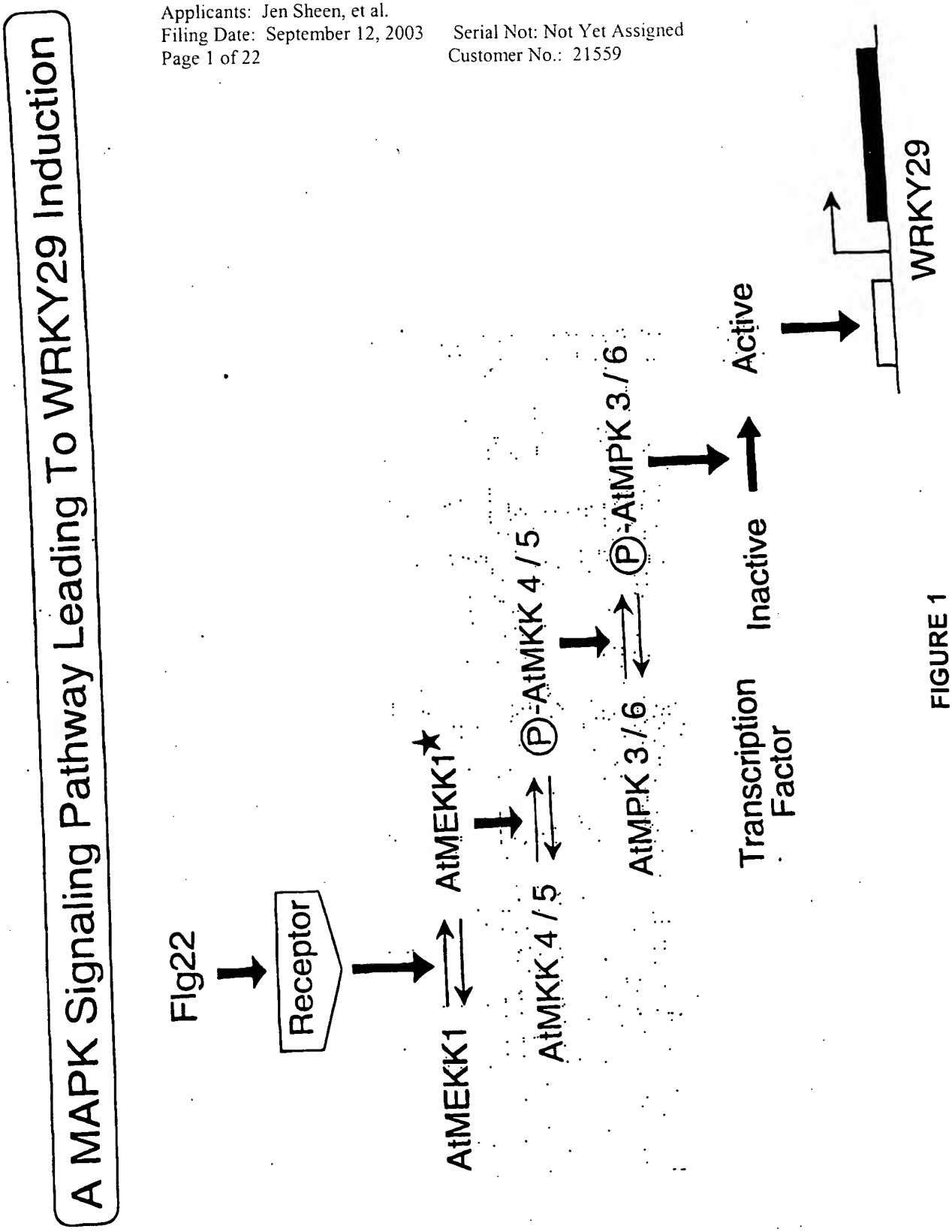

A MAPK Signaling Pathway Leading To WRKY29 Induction
Flg22
Receptor
AtMEKK1
AtMEKK1*
AtMKK 4 / 5
Ⓟ-AtMKK 4 / 5
AtMPK 3 / 6
Ⓟ-AtMPK 3 / 6
Transcription Factor
Inactive
Active
WRKY29

FIGURE 1

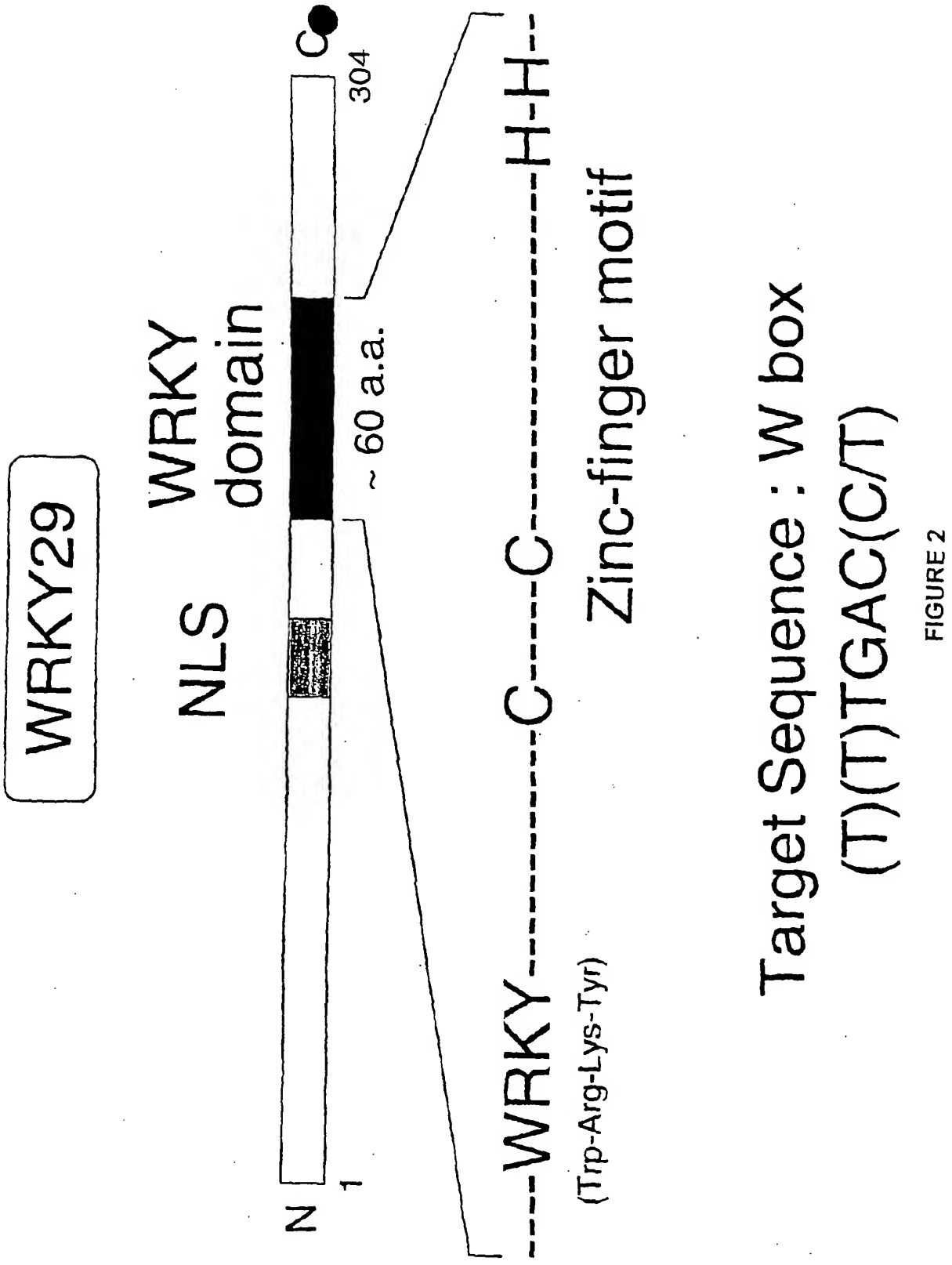

WRKY29
NLS
WRKY domain
N
1
~ 60 a.a.
C
304
---WRKY--------C----C----------H-H--
(Trp-Arg-Lys-Tyr)
Zinc-finger motif
Target Sequence : W box
(T)(T)TGAC(C/T)

FIGURE 2

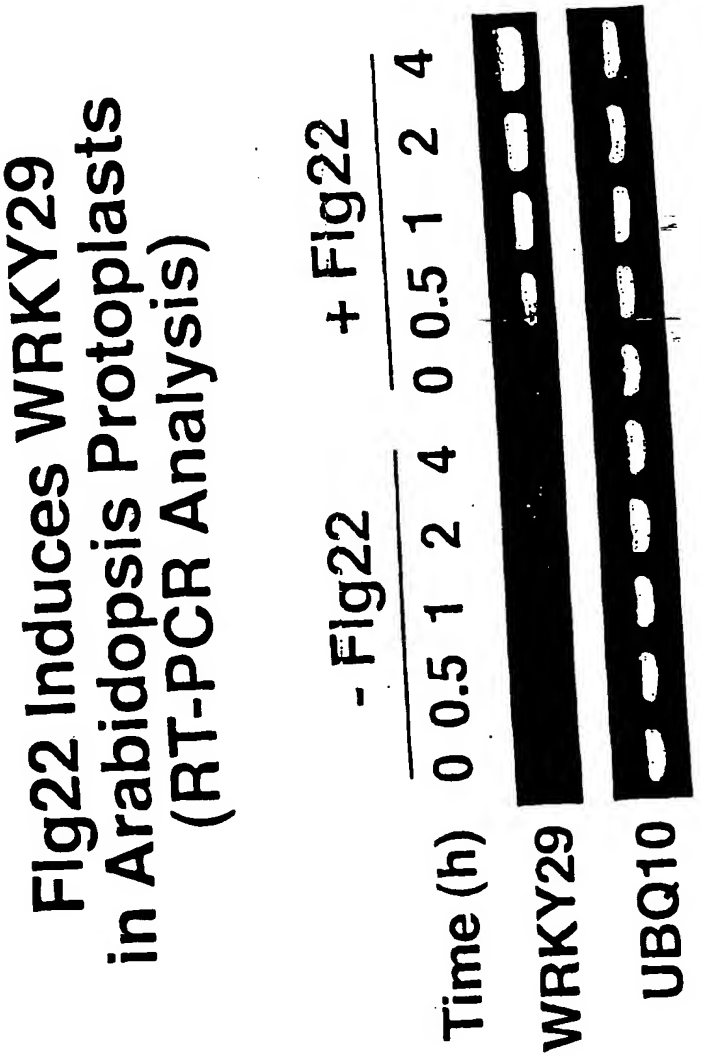

Flg22 Induces WRKY29
in Arabidopsis Protoplasts
(RT-PCR Analysis)
- Flg22
+ Flg22
Time (h) 0 0.5 1 2 4 0 0.5 1 2 4
WRKY29
UBQ10

FIGURE 3

MKK4 (cDNA accession number: AB015315)

Wild-type cDNA sequence from start to end codons (1101 base pairs including the end TAG):

atgagaccgattcaatcgcctccaggagtttccgttccggtgaaaagccgtccccgtcg
ccgtcctgatcttaccttaccgcttcctcaacgcgatgtttctctcgctgtacctcttc
ctctcccacctacttccggtggttccggtggctctagtggatctgcgccgtcttctggt
ggttcggcgtcttcaacgaacactaacagctccatagaagcgaagaactattcggattt
agtgagaggtaaccgtatcggaagcggagcaggtggaacggtatacaaagtgattcacc
gtccgagttctcgtctatatgcacttaaggtgatatacggtaaccacgaggagactgtg
agacgtcagatctgtagagagatcgagattttacgagatgtgaatcatccaaacgttgt
gaaatgtcacgagatgtttgatcagaacggtgagatccaggttttgcttgagtttatgg
ataaaggttctttagaaggtgctcatgtgtggaaagagcaacaattagctgatctatct
cgtcagattcttagtggtttagcttatctccatagccgtcacatagttcatcgtgatat
caaaccatcgaatcttttgataaactctgctaaaaacgttaagattgctgattttggag
ttagtaggatcttggctcagatatggatccgtgtaattcatctgttggaaccattgct
tatatgagtcctgagaggattaacactgatttgaatcagggaaagtatgatggttatgc
tggagatatttggagcttaggtgttagcattttggagttttacttggggaggtttcctt
tccctgtgagtagacaaggtgattgggctagtcttatgtgtgccatttgtatgtctcag
cctccagaagctccagcgactgcgtcgccggagtttcggcattttatctcgtgttgctt
gcagagagaaccggggaaaaggaggagtgctatgcagctattgcagcatcctttcatat
taagagcaagtccgagccagaacaggtctcctcagaatctacatcaactcttgcctcct
cctcgtcctctgtcctcgtcttcttctccaaccacatag **(SEQ ID NO.:3)**

Wild-type protein sequence (366 aminoacids):

MRPIQSPPGVSVPVKSRPRRRPDLTLPLPQRDVSLAVPLPLPPTSGGSGGSSGSAPSSG
GSASSTNTNSSIEAKNYSDLVRGNRIGSGAGGTVYKVIHRPSSRLYALKVIYGNHEETV
RRQICREIEILRDVNHPNVVKCHEMFDQNGEIQVLLEFMDKGSLEGAHVWKEQQLADLS
RQILSGLAYLHSRHIVHRDIKPSNLLINSAKNVKIADFGVSRILAQTMDPCNSSVGTIA
YMSPERINTDLNQGKYDGYAGDIWSLGVSILEFYLGRFPFPVSRQGDWASLMCAICMSQ
PPEAPATASPEFRHFISCCLQREPGKRRSAMQLLQHPFILRASPSQNRSPQNLHQLLPP
PRPLSSSSSPTT **(SEQ ID NO.:4)**

FIGURE 4

Mutations rendering MKK4 constitutively active:

- modify Threonine (T) 204 to Aspartic Acid (D) by changing codon ACT into GAT

- modify Serine (S) 230 to Glutamic Acid (E) by changing codon TCA into GAA

The mutations were done by PCR using the primers (mutated base pairs in lower case, both are from 5' end to 3' end):

CTTGGCTCAGgaTATGGATCCGTGTAATgaATCTGTTGGAAC
TCCAACAGATtcATTACACGGATCCATAtcCTGAGCCAAG **(SEQ ID NO.3)**

So the sequences after mutations are:

MKK4act mutant sequence from start to end codons (1101 base pairs including the end TAG):

atgagaccgattcaatcgcctccaggagtttccgttccggtgaaaagccgtccccgtcgccgtcctgatct
taccttaccgcttcctcaacgcgatgtttctctcgctgtacctcttcctctcccacctacttccggtggtt
ccggtggctctagtggatctgcgccgtcttctggtggttcggcgtcttcaacgaacactaacagctccata
gaagcgaagaactattcggatttagtgagaggtaaccgtatcggaagcggagcaggtggaacggtatacaa
agtgattcaccgtccgagttctcgtctatatgcacttaaggtgatatacggtaaccacgaggagactgtga
gacgtcagatctgtagagagatcgagattttacgagatgtgaatcatccaaacgttgtgaaatgtcacgag
atgtttgatcagaacggtgagatccaggttttgcttgagtttatggataaaggttctttagaaggtgctca
tgtgtggaaagagcaacaattagctgatctatctcgtcagattcttagtggtttagcttatctccatagcc
gtcacatagttcatcgtgatatcaaaccatcgaatcttttgataaactctgctaaaaacgttaagattgct
gattttggagttagtaggatcttggctcaggtatggatccgtgtaatgaatctgttggaaccattgctta
tatgagtcctgagaggattaacactgatttgaatcagggaaagtatgatggttatgctggagatatttgga
gcttaggtgttagcattttggagttttacttggggaggtttcctttccctgtgagtagacaaggtgattgg
gctagtcttatgtgtgccatttgtatgtctcagcctccagaagctccagcgactgcgtcgccggagtttcg
gcattttatctcgtgttgcttgcagagagaaccggggaaaaggaggagtgctatgcagctattgcagcatc
ctttcatattaagagcaagtccgagccagaacaggtctcctcagaatctacatcaactcttgcctcctcct
cgtcctctgtcctcgtcttcttctccaaccacatag **(SEQ ID NO.:6)**

MKK4act mutant protein sequence (366 aminoacids):

MRPIQSPPGVSVPVKSRPRRRPDLTLPLPQRDVSLAVPLPLPPTSGGSGGSSGSAPSSGGSASSTNTNSSI
EAKNYSDLVRGNRIGSGAGGTVYKVIHRPSSRLYALKVIYGNHEETVRRQICREIEILRDVNHPNVVKCHE
MFDQNGEIQVLLEFMDKGSLEGAHVWKEQQLADLSRQILSGLAYLHSRHIVHRDIKPSNLLINSAKNVKIA
DFGVSRILAQSMDPCNESVGTIAYMSPERINTDLNQGKYDGYAGDIWSLGVSILEFYLGRFPFPVSRQGDW
ASLMCAICMSQPPEAPATASPEFRHFISCCLQREPGKRRSAMQLLQHPFILRASPSQNRSPQNLHQLLPPP
RPLSSSSSPTT **(SEQ ID NO.:7)**

FIGURE 5

MKK5 (cDNA accession number: AB015316)

Wild-type cDNA sequence from start to end codons (1047 base pairs including the end TAG):

atgaaaccgattcaatctccttctggagtagcttcacctatgaagaaccgtttacgcaa
acgtcctgacctaagcttaccactcccacaccgcgacgtcgctctcgccgtacctctcc
ctctcccacctccttcttcctcttcatccgctccggcgtcttcctccgcgatctcaacc
aacatctccgccgctaaaagcttatccgagctagaacgagtgaaccgaatcggaagcgg
agccggaggaacggtttacaaagtaatccacactccgacgtcacgtcctttcgctctca
aagtgatttacggaaaccacgaagataccgtgagacgtcagatctgtagagagatcgag
atcttaagaagtgttgatcatccaaacgttgtgaaatgtcacgatatgtttgatcataa
cggtgagatccaggttttgcttgagtttatggatcaaggatctcttgaaggagctcata
tatggcaagaacaggaattagctgatctctctcgtcagattcttagtggattagcttat
cttcatcgtcgtcatatcgttcatcgtgatatcaaaccttcgaatctccttataaactc
agctaaaaatgtgaaaattgctgattttggtgtgagtaggatcttggcacaa[N]aatgg
atccttgtaat[c]catctgttggtactattgcttatatgagtcctgagaggattaatact
gatttgaatcatggtcgttacgatggttatgctggagatgtttggagtttaggtgttag
tatcttggagttttacttggggaggtttccttttgctgtgagtagacaaggtgattggg
ctagtcttatgtgtgctatttgtatgtctcagccacctgaagctccggctacggcgtct
caggagtttcgtcactttgtttcttgttgtttacagagtgatcctcctaagagatggtc
agctcaacagcttttgcagcatcctttcatacttaaagctaccggtggtcctaatctcc
gtcaaatgttgccgccgcctcgtcctcttccttctgcctct[a]ag (SEQ ID NO.:8)

Wild-type protein sequence (348 aminoacids):

MKPIQSPSGVASPMKNRLRKRPDLSLPLPHRDVALAVPLPLPPPSSSSSAPASSSAIST
NISAAKSLSELERVNRIGSGAGGTVYKVIHTPTSRPFALKVIYGNHEDTVRRQICREIE
ILRSVDHPNVVKCHDMFDHNGEIQVLLEFMDQGSLEGAHIWQEQELADLSRQILSGLAY
LHRRHIVHRDIKPSNLLINSAKNVKIADFGVSRILAQ[T]MDPCN[S]SVGTIAYMSPERINT
DLNHGRYDGYAGDVWSLGVSILEFYLGRFPFAVSRQGDWASLMCAICMSQPPEAPATAS
QEFRHFVSCCLQSDPPKRWSAQQLLQHPFILKATGGPNLRQMLPPPRPLPSAS (SEQ
ID NO.:9)

FIGURE 6

Mutations rendering MKK5 constitutively active:

- modify Threonine (T) 215 to Glutamic Acid (E) by changing codon ACA into GAA

- modify Serine (S) 221 to Glutamic Acid (E) by changing codon TCA into GAA

The mutations were done by PCR using the primers (mutated base pairs in lower case, both are from 5′ end to 3′ end):

CTTGGCACAAgAATGGATCCTTGTAATgaATCTGTTGGT
ACCAACAGATtcATTACAAGGATCCATTcTTGTGCCAAG **(SEQ ID NO.:10)**

So the sequences after mutations are:

MKK5act mutant cDNA sequence from start to end codons (1047 base pairs including the end TAG):

atgaaaccgattcaatctccttctggagtagcttcacctatgaagaaccgtttacgcaa
acgtcctgacctaagcttaccactcccacaccgcgacgtcgctctcgccgtacctctcc
ctctcccacctccttcttcctcttcatccgctccggcgtcttcctccgcgatctcaacc
aacatctccgccgctaaaagcttatccgagctagaacgagtgaaccgaatcggaagcgg
agccggaggaacggtttacaaagtaatccacactccgacgtcacgtcctttcgctctca
aagtgatttacggaaaccacgaagataccgtgagacgtcagatctgtagagagatcgag
atcttaagaagtgttgatcatccaaacgttgtgaaatgtcacgatatgtttgatcataa
cggtgagatccaggttttgcttgagtttatggatcaaggatctcttgaaggagctcata
tatggcaagaacaggaattagctgatctctctcgtcagattcttagtggattagcttat
cttcatcgtcgtcatatcgttcatcgtgatatcaaaccttcgaatctccttataaactc
agctaaaaatgtgaaaattgctgattttggtgtgagtaggatcttggcacaaAcaatgg
atccttgtaatgaatctgttggtactattgcttatatgagtcctgagaggattaatact
gatttgaatcatggtcgttacgatggttatgctggagatgtttggagtttaggtgttag
tatcttggagttttacttggggaggtttccttttgctgtgagtagacaaggtgattggg
ctagtcttatgtgtgctatttgtatgtctcagccacctgaagctccggctacggcgtct
caggagtttcgtcactttgtttcttgttgtttacagagtgatcctcctaagagatggtc
agctcaacagcttttgcagcatcctttcatacttaaagctaccggtggtcctaatctcc
gtcaaatgttgccgccgcctcgtcctcttccttctgcctctTag **(SEQ ID NO.:11)**

MKK5act mutant protein sequence (348 aminoacids):

MKPIQSPSGVASPMKNRLRKRPDLSLPLPHRDVALAVPLPLPPPSSSSSAPASSSAIST
NISAAKSLSELERVNRIGSGAGGTVYKVIHTPTSRPFALKVIYGNHEDTVRRQICREIE
ILRSVDHPNVVKCHDMFDHNGEIQVLLEFMDQGSLEGAHIWQEQELADLSRQILSGLAY
LHRRHIVHRDIKPSNLLINSAKNVKIADFGVSRILAQAMDPCNESVGTIAYMSPERINT
DLNHGRYDGYAGDVWSLGVSILEFYLGRFPFAVSRQGDWASLMCAICMSQPPEAPATAS
QEFRHFVSCCLQSDPPKRWSAQQLLQHPFILKATGGPNLRQMLPPPRPLPSAS **(SEQ ID NO.:12)**

FIGURE 7

Alignment of MKK4 and MKK5 wild-type:

```
MKK4 MRPIQSPPGVSVPVKSRPRRRPDLTLPLPQRDVSLAVPLPLPPTSGGSGG
MKK5 MKPIQSPSGVASPMKNRLRKRPDLSLPLPHRDVALAVPLPLPPPS-----

MKK4 SSGSAPSSGGSASSTNTNSSIEAKNYSDLVRGNRIGSGAGGTVYKVIHRP
MKK5 SSSSAPASS-SAISTNIS---AAKSLSELERVNRIGSGAGGTVYKVIHTP

MKK4 SSRLYALKVIYGNHEETVRRQICREIEILRDVNHPNVVKCHEMFDQNGEI
MKK5 TSRPFALKVIYGNHEDTVRRQICREIEILRSVDHPNVVKCHDMFDHNGEI

MKK4 QVLLEFMDKGSLEGAHVWKEQQLADLSRQILSGLAYLHSRHIVHRDIKPS
MKK5 QVLLEFMDQGSLEGAHIWQEQELADLSRQILSGLAYLHRRHIVHRDIKPS

MKK4 NLLINSAKNVKIADFGVSRILAQTMDPCNSSVGTIAYMSPERINTDLNQG
MKK5 NLLINSAKNVKIADFGVSRILAQTMDPCNSSVGTIAYMSPERINTDLNHG

MKK4 KYDGYAGDIWSLGVSILEFYLGRFPFPVSRQGDWASLMCAICMSQPPEAP
MKK5 RYDGYAGDVWSLGVSILEFYLGRFPFAVSRQGDWASLMCAICMSQPPEAP

MKK4 ATASPEFRHFISCCLQREPGKRRSAMQLLQHPFILRASPSQNRSPQNLHQ
MKK5 ATASQEFRHFVSCCLQSDPPKRWSAQQLLQHPFILKATG----GP-NLRQ

MKK4 LLPPPRPLSSSSSPTT     (SEQ ID NO.:13)
MKK5 MLPPPRPLPSAS----     (SEQ ID NO.:14)
```

FIGURE 8

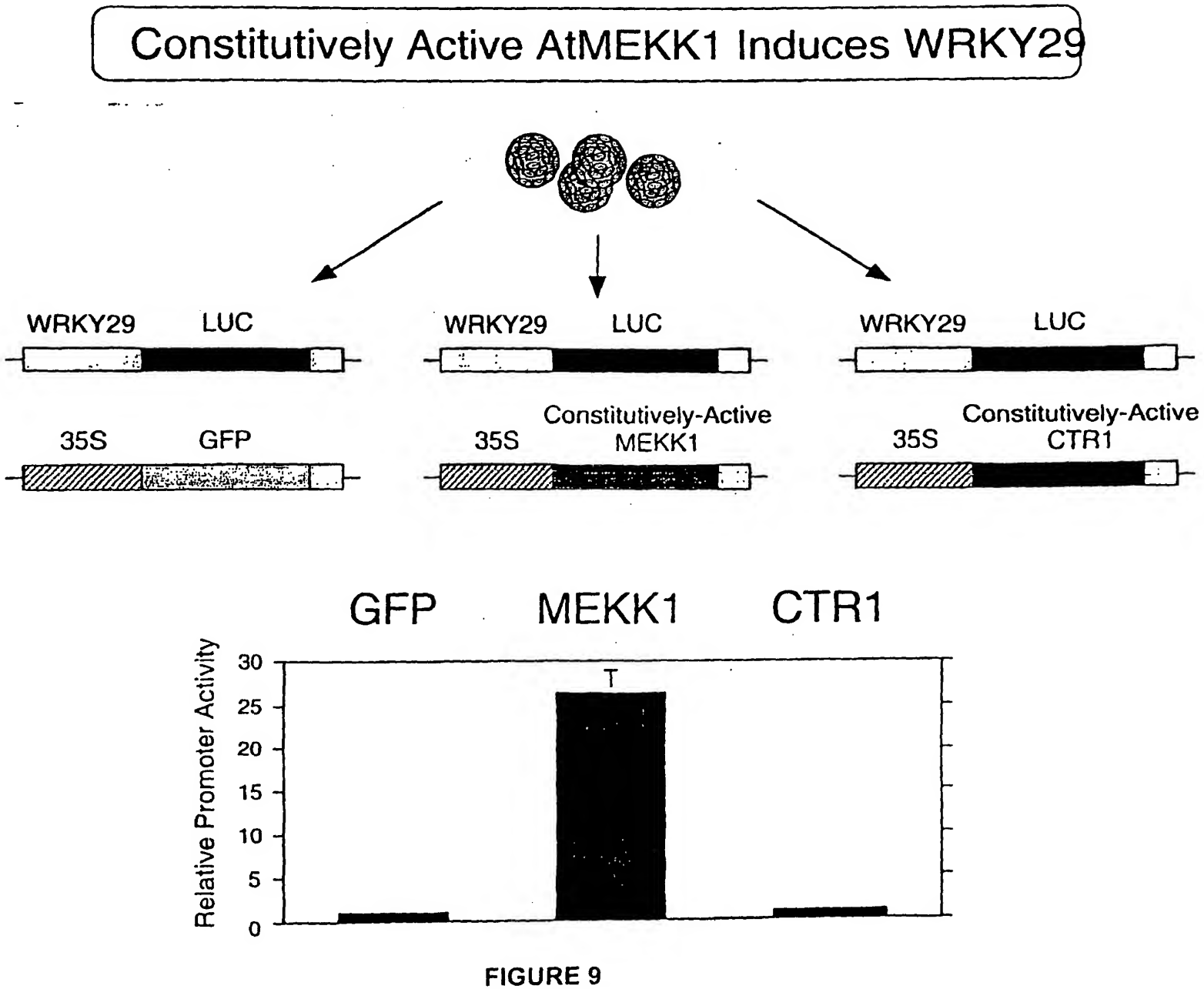

Constitutively Active AtMEKK1 Induces WRKY29
WRKY29
LUC
WRKY29
LUC
WRKY29
LUC
35S
GFP
Constitutively-Active
35S
MEKK1
Constitutively-Active
35S
CTR1
GFP
MEKK1
CTR1
Relative Promoter Activity
30
25
20
15
10
5
0
T

FIGURE 9

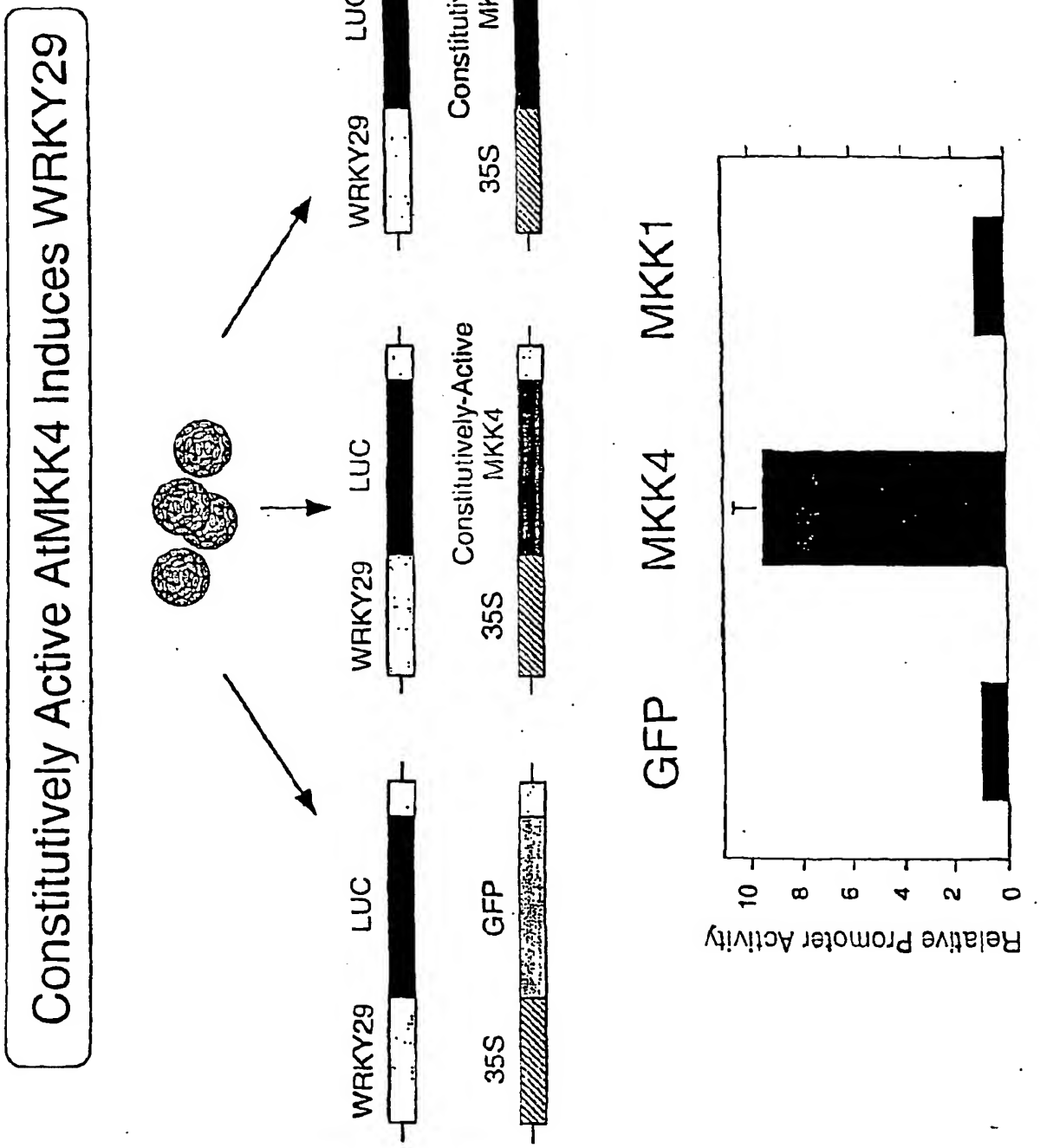

Constitutively Active AtMKK4 Induces WRKY29
WRKY29
LUC
35S
GFP
WRKY29
LUC
35S
Constitutively-Active MKK4
WRKY29
LUC
35S
Constitutively-Active MKK1
GFP
MKK4
MKK1
Relative Promoter Activity
0
2
4
6
8
10

FIGURE 10

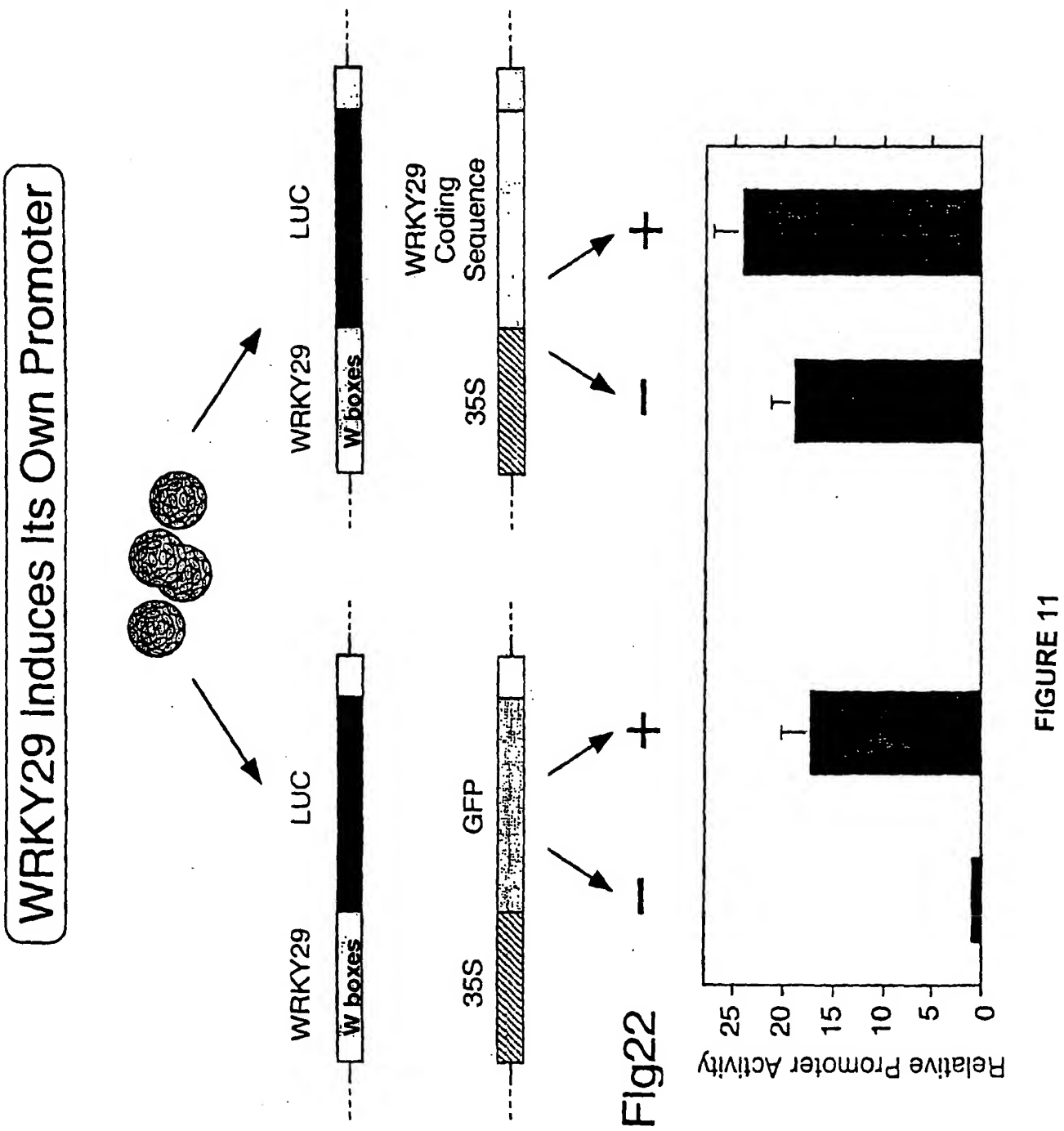


Fig22

FIGURE 11

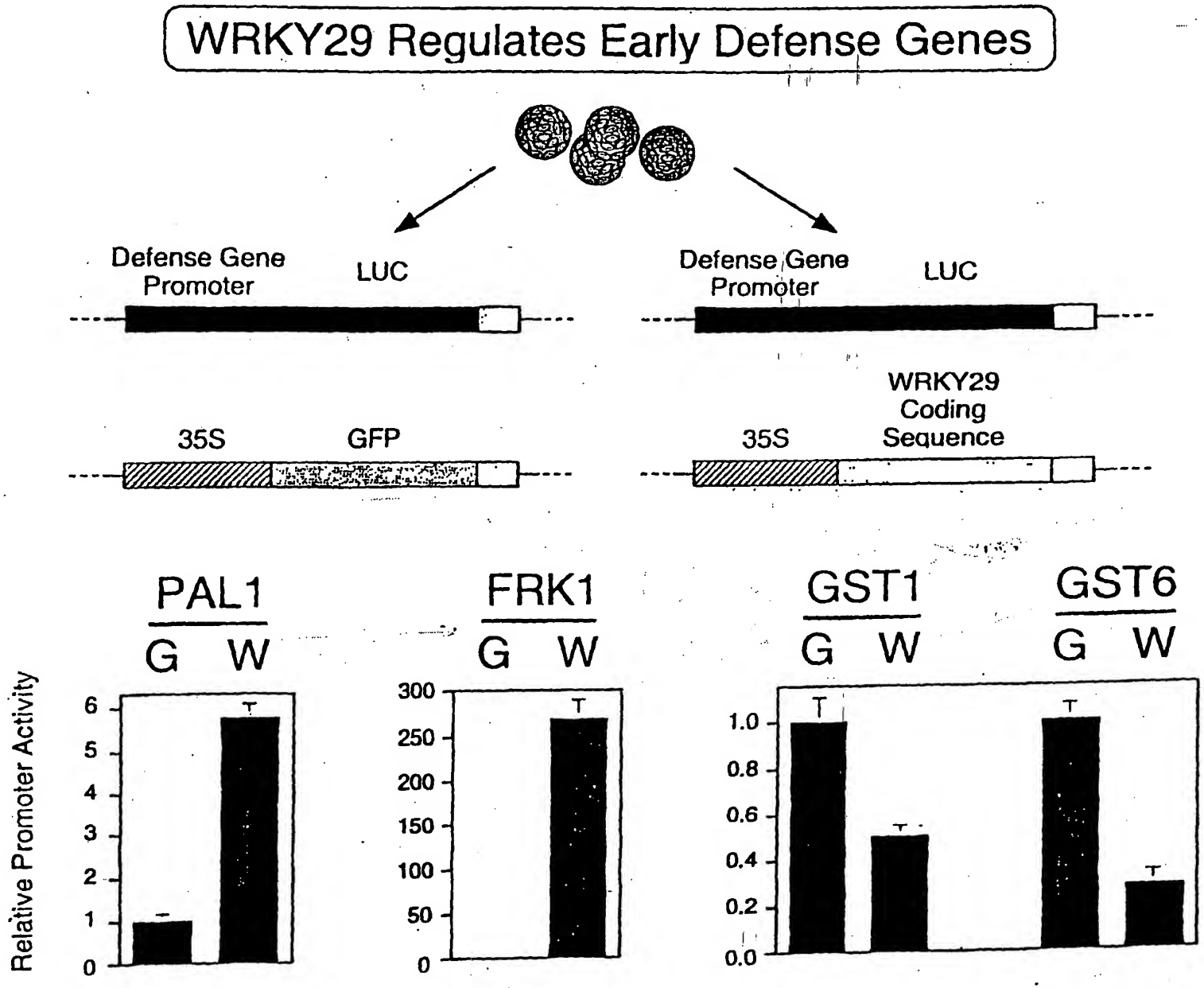

WRKY29 Regulates Early Defense Genes
Defense Gene Promoter
LUC
35S
GFP
Defense Gene Promoter
LUC
35S
WRKY29 Coding Sequence
PAL1
G W
FRK1
G W
GST1
G W
GST6
G W
Relative Promoter Activity
0
1
2
3
4
5
6
0
50
100
150
200
250
300
0.0
0.2
0.4
0.6
0.8
1.0

FIGURE 12

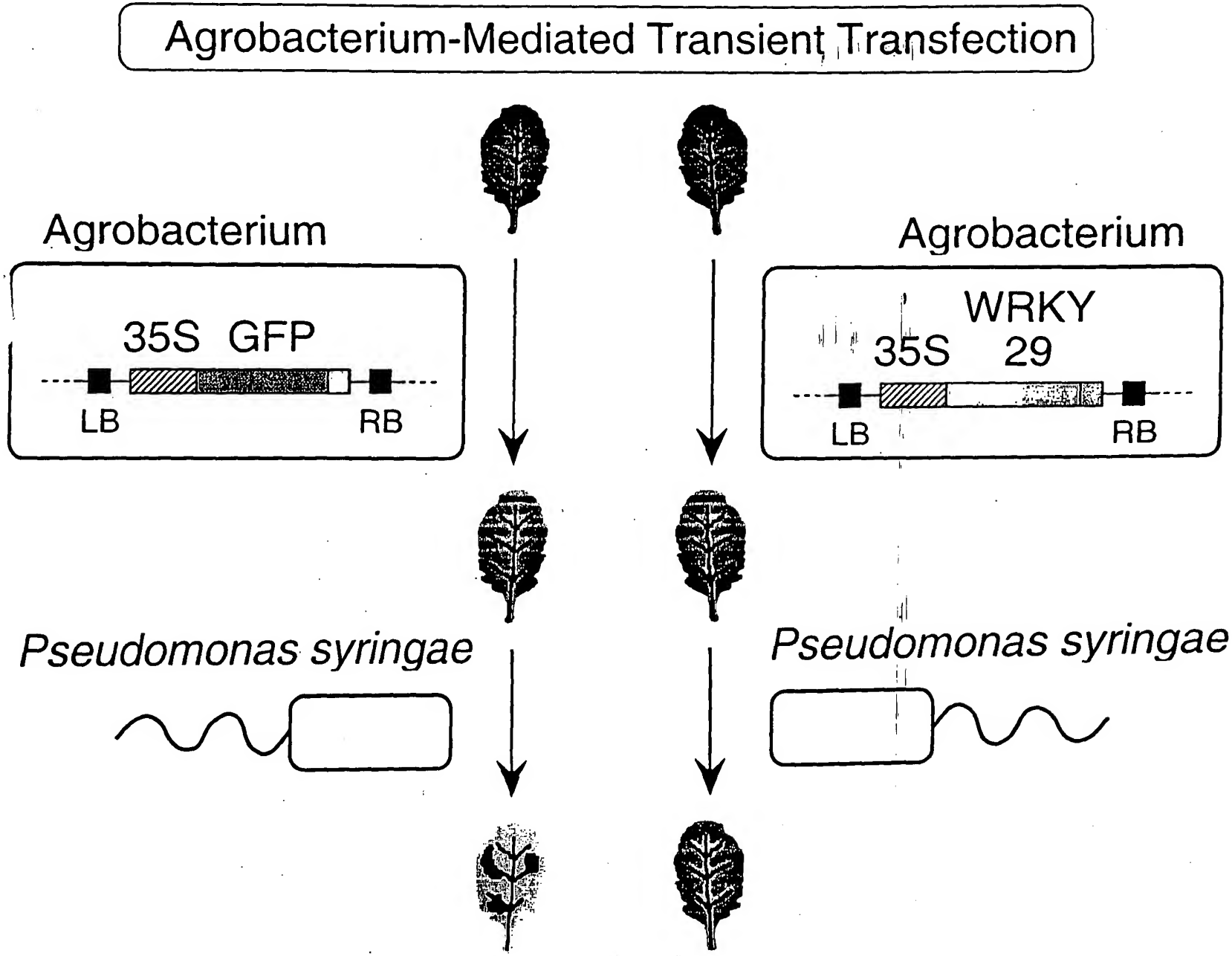

Agrobacterium-Mediated Transient Transfection
Agrobacterium
35S GFP
LB
RB
Agrobacterium
WRKY
35S 29
LB
RB
Pseudomonas syringae
Pseudomonas syringae

FIGURE 13

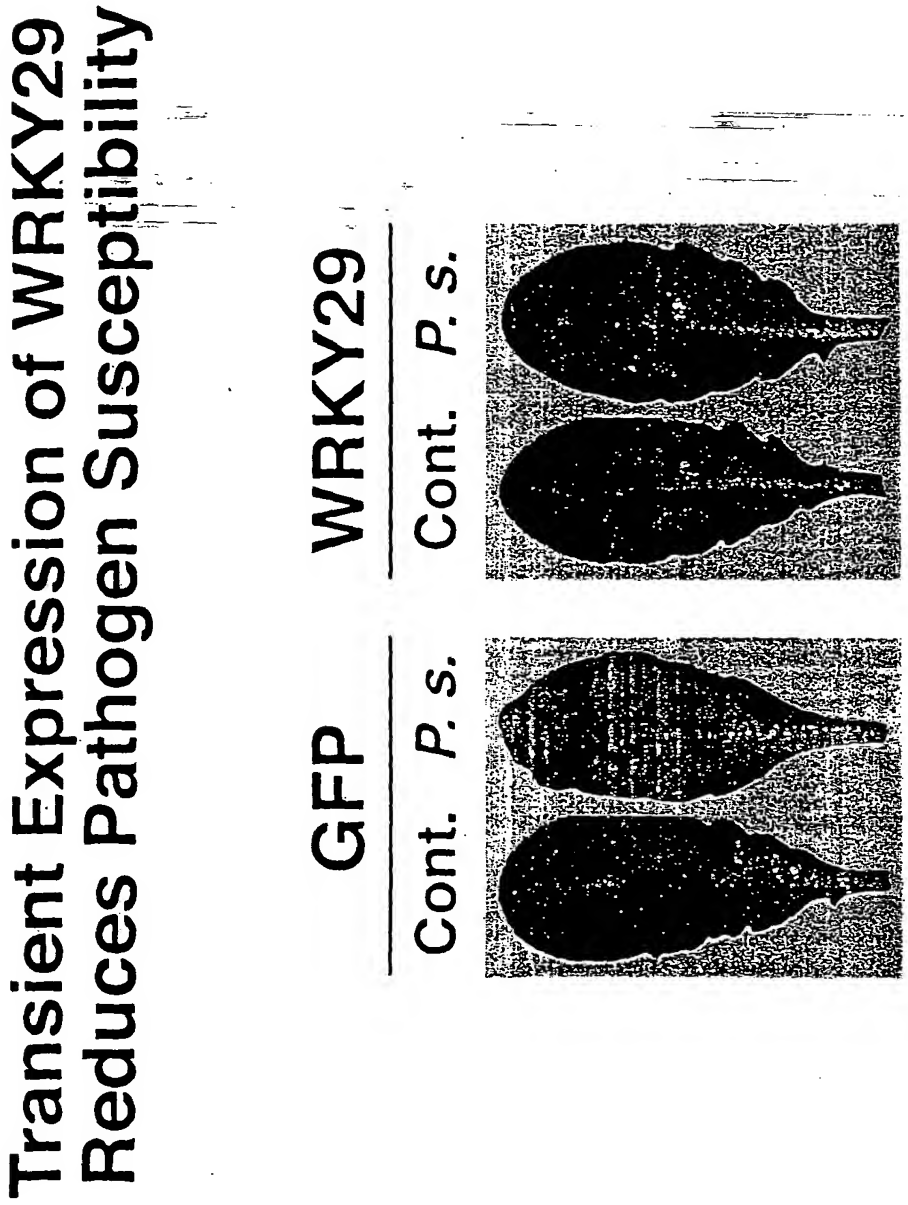

Transient Expression of WRKY29
Reduces Pathogen Susceptibility
GFP
Cont.
P. s.
WRKY29
Cont.
P. s.

FIGURE 14

WRKY29 promoter fragment

5'-
TCGTCCATGATGGACATATATGTGACTGCGTATTTACACACACCGCACGTATGCTTATTTCACA
CGTTAGAAGAAGAATTCAAAGAAGTCGGTTCTATTTGTATTCTTGTGAGATCATCAATATGAC
AATATCGTTCTATTAATATACGTATAATTCATATGTTGTCATGGTTTCACATACCATGTCGACA
GTCGACGTACGTACAAAAGTATAAATAGTATGAATCTAATAACAGCACCAAGATTGAAGTTC
ATCTTCTAATCAAAACTATCATAAAGTGGTTTCAAAATAGTGTTTTTTCTGATGAAACTATAAC
TGAGTTATAATCAATCCGAAATTATATAACTAATTATATTTGGGAACTAGATAAACGCAAAAA
CATGAGCAGTTTCTTATTTTTTTTGTCCAGATTTAAAATTTGGAGTGTTAAAATATACGGAGTG
TTACACAATGAAAACACAAGAAGTCAAGAACCCATAAGTTATTTTAATTAATAATATTGTATT
TAAAGTGATTATTAAAAAATAATGTAAAAACTGATTATTTGTTGACAAAAAACAGTTAGTTAT
AGTTAAATAGTATTGATGCATATATATACTATCTCATTATTTTGGTATTACTCAGTACTCACAT
CTTTAATAAAGACAAAGATAGTTAGTGTATAATTCAAATCGAACTCACAGAAGTCAATAAGC
GCGTAAAAATACAAAAATATCTGGCAGACTTTAGCAAGGTTTGTTTTCCAACAGAAATGGTCA
TTTCAGAATCATTTACATATCCATATATATAGCTCTTAAATGGTATATATTGGGTAATGGGTAT
TCGTTTAAATAATTTTGTTTTCTGTAAATTTCAAATATTAATCTGATCAGTTTATCCATGTGTGT
ATATTTAGTGTATTATCATCAATATATGACATAGACAGACTTTCAAGTTGGTGCAAGAGGGGA
TGAAAATTTCTTCCCAGTTGCAAGAGTAAGCTGACTAGCATTTTTTTTTTATATATAATTTATTT
CTCAAATGGTTTTTATTATTGTTTTGTTGACTTTAAGTTTTTGCCTTTTATGGGACTGCAATCAC
CCGTGCCAACTTTTAATCTCCATCGCCTAAAAAAGAAAGAAAAGGCTACCATTATGGACCGAA
ATATTTAAGACCATAATACAAAATTATACGAATATTTTCTGTAACTTATATATATGATCATTTG
ACAAAGCAAAGTCAATCAAATAAACTTCAAAGAAATTATGAGCTTATAATAAGTTTGATAGT
GTTAAATATAATCAAATCATTAAATTTAGTATTTATTTCATCTCGGTTTCCATTTGATAGATAG
ATAAATGAAAGATAGCATCGCCAATAATGAAAAAACTTTATTTGATGGCAATACTTTGTTACA
TCATTTCTGTTTTCTTAATTTCATGTCGAAATATTGCCATGATTGTGTTCAACATAACTAGTTTT
GAGGTAACAAGTTAAAAATTTGTTATATTTTTTGAATATGTTATTCAGTTGAAAGTCATTTAGA
TGTAAGTAAAAACAAACATAAGAAGTTAACATATCAATATTAACACAGCGAATAATCATTATT
ACAAAAAAAAAGCAAAAAAATAGAAGAAGATATTATATATTGGAGAATCTTTCTTTAGTCTTA
GTTGGGAAGATTTTGTGCTATGGGATTAAAGGTATCCATCCCTATTCTATGATAGAGGCGTGG
GGTTATTGGACCAATCTATATATATTACCACAAGGCTTAAGATGAAGTGATAATACAGTATTA
TTAATACCCTCCCAAATTATTTTTAAATATTTATCAAAAGAAGCTTACGGTATAGATCATACTT
GCAGCATTATTCTATAAGTTTATTTAATTTCAGTGGCTCGTTACGTGAACACAAGGTAAGCTA
ATAGACTTACGTGCCCCATTAAACACATACATAATTATACAAGTATCATGAAACTAGTGACAA
AACCTCGATCAAATAAAGAAATTACCATGACGACAAAAGATAATTAAAAAAAAAAACTACTAT
ATGTCATACTCATGCATATGCATGTACAAATGCCGCTTTAAATATTTAATTTAGTTAAAGCAAT
GATATTTAAATTCTCTCTACTTCATATATATTCCAAAAGACATATTGTCAAATTCCTTTTTTTAG
TTATATATAATCATATATTCATATTGTTATATTTTCAATATTTAATAGTAAGATGGACTTTCCTG
AATGTTGTGTATGATTTATAATTTGAGATATTTTGTCGGAGATGGATATTTGACAAGTTAATGT
TACTTTATTAAAATTTTCTAAACATTTAGGTACGAATTGACTTTTTCAAAAGTCAACACAATAA
ATTTTAAAAGTTTAATGACTTAACGGGTTCACATGGGAAACGAAAACACCCTAAACCACAAA
CAATCTAATCTTATTTCCTTCTTTATATAAACCGCTGTTTCCCAAAAGGCTTGTTCTCGTCATAT
GTACTTGTACACCAACCCACCAAAAGAGATAAAAGAGGAAACAAAAACTCGAAAAGAGAGA
GATATATGGGTGAGGTGGCTTAT - 3' **(SEQ ID NO.: 15)**

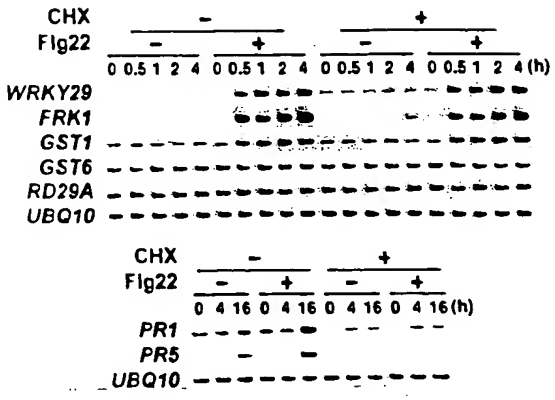
Figure 15

WRKY22 Promoter Fragment

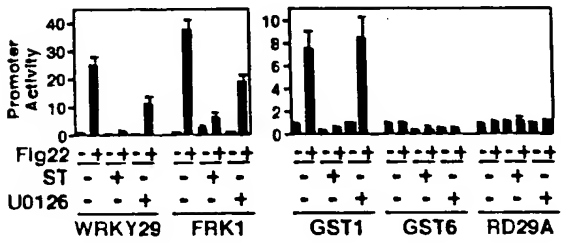
5' -
CTGACAGTGAACTTCATTGTTCAAGCGAGGTGAGTTTCCTATTTTTCTTCTTCTCCTTTCAATTA
AAATTTCAGGGTTTATGATCTCTAGGGTTTAGGTTTTATTTTCTTAAACTAAACCCTAAATTCT
TTTTCTTCTTCTTTTTCTTGTAATTTCCAGATGCACTGCGAACGCTAGAGGAGGTGCGATATCG
AAGAGGAAGCGTTATACAGGATCATGGGACCAAAATATATCGTATAGATTCGGTTCTTGTTCT
TCTATACCTTATGAGAGTAGAAGTTTTTCTCTTCAAGAGAAAAAAAAAAAAAAGAAAAAAAA
AAAAGAAGAGTAGAAATTTCTCTGTGTTTTTTTTTACCAACAAGACACAAATGAAACTGGTCC
AAAAGGAGTGTGTATAATCTCTGTGGAGACATAACTAATACGTTGATGAATTTCAAGAATACT
TGGATTATATAGATTAACCCTGACTCCCTTAGATAGAGATCGAAATCGGGTGGTGATTTCTGA
GACCATACAAGTTCTGATCAGATTACTACTAAGTAAATCTTAATTATTAGACTGTTTTTAATGG
ATTTTTCTGCTCTAATGATAACGTAATGAGATTTTTTTTTTTTTTTTGTATGTTTGGCTTGCAGA
CCCGGGTAATGAGAAGTTTGGTAAGAGCAAAAGGCACTAATCTCACGTAAGAAAACACTTTT
TTCATCAACCATGTATATAATCATGTCGGTTTACATAAACCGTATCGTCTATTCAAGAATTTAG
TTTTGTATAATTATAATATTTTTTTCAGACTACTTTTCAATTAAGCATCTTTTTCTTGGATTTTTT
TTTCACAAAGGGAGAGCTTTAACTTTTTGCATTAACTTATATATTTTAAATTATACATGCATGC
ATACCGACTTATATAAATCATATGGTCAATATGAGACTTTTGATTTATATTATTTGTCAACTAA
GCATCTTTTCAGATGAGGTTCATGCACCTTTGTTAGAATTATCGGACCAGAAGATCACATCAA
CGTTTACCAAATCAACAAAAAAATCCAATCCGTCCAAAAAATTTGGAAACTGTTTGAAAGATT
CGAAATGTTGGAGCAAGGATACTCAGTTCCAATCTCTGAGCAGAATCTGATATGACTCATCTA
CTCATAAGACTTTGCGAGATAGACCGGTACAAAACCGTTTCCAAGGGTTCATAATATATGGAT
TAATGTGAGTTATTGTGGACGTTGTGGTTGTAGAAGCCGCGGTAGTCGTGGAAACACTAATTA
GTTATCTCCTGTAAGCTATTTTTATTTTTTTTCCTCACTTCCTCTTCCTCGCAGCTATGTATAATT
TTGGTTGGTTATCTCCAAAACTTTTTATGGTCAAACAATTTTGAGAAAGTAATTTGGAAAGAA
AAAAGGTTTAAGAATATCTTTTTATCGTCAAGTCCTCCTCCAAATTACTTCCTTAAAACTGTTT
GACCATAAAAAGTCATAGCAAGGTATTAGTTATTCTAATTTAAATTAAACGCCTTTTTATCAA
CAACAAAAAAAAGAAGAAGATTTGATATGTTGAAAAGTATTAGGGACGCTTATTAGGGCAGT
ATTCCTAGTTATTGCATTTTCTTTCGGTCATTCGACCTTAGGATCATACCTCAATCTGTATGACT
GTATTCGCCATGTGAATTCCAATATTACATAGTGACCAAATTTGATATCCAACTAAAAGTCGA
TCTTTGATCTAAACGAAATGACAACTATTTGGTTAGTGATTGCAGGTTGGAAAGATTTACCTTC
TAGACCTGTCTTACGAAGCTAGTATTCTAAAGTAATCTTCATAAACCGAATTCAGAAACAAAA
AAAGAAAAGGAGTCCAAAATTGTATGATCATACATTAATATCAGAATAGTCTCTTTTGTTAAA
TAAATATCTGAAGAATATATATCTCTTTGATTATTTTGTGGATGGCAATGAAACTAAGAATAT
ATATTCATTGACTTAGAAGTCGACAAAAAAAAAATAAAAAAATTATTGACTTAATTACTAGTTG
ACCAATATATATATTATTAAAAGAACATATTGTATCGTTGAAAGCGGATCATCGGGTTTTAAA
AGAAAAACACATCGTTGAAACTTGAAAGTGATGACTAATAAAAAGATCTAAACGTGTCCGGT
CACCTACCAATGTGGTTTTGCAAATTATTGTCAAGTACCTTGACTATATTAAATAAAAAAATTC
ACCGTAACACATTGATATTCAACTGATTCCTAAAAAAATATACAAACTATTGGGAGTTGTGAG
ATTTTTTATATCAGTGTTGGTCTCTTTACATTTGTGATGTGGTGTTATAGCATATATAGTAATA
AACTCAAAAGGAAATTAGATGTGTTTTGACCATTTATTAAAATGAACCTTTTCTTGTCAAACAT
TTGAAAAATACTAGTTTTTTTTTTTGGCAACGTTGTAAATAATAGTTAAAAATAGATTTTAAGT
CTCGTTTTTTTATGCATATAGTTTCATTCGCTTTATTAGACTCAAATATACTTTTAATTAAATTT
TGCAGAGAATTAAAGGTAATCATTTGCCAAGGAAAAACCATGCAAATATGCAATAAGTAGAA
ATAATGTTAATGAGAGTAAGCGTTGACATATATTACGTCCTGGTCCGAACATTCTTAAAGTTG
CGTAACACTAATAACCTTAGAAGATGGTTGGTTGACTATCAACATCTTATTGACCAAATGTTTT
TTTTTTTTTAATTATAAAACAGTTGCTCATTGCTCTAGCCCAGAGAAAGCAGCTCAATTAAGTA
A - 3' **(SEQ ID NO.:16)**

Figure 16

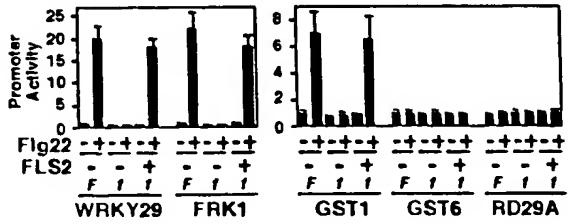
17 A



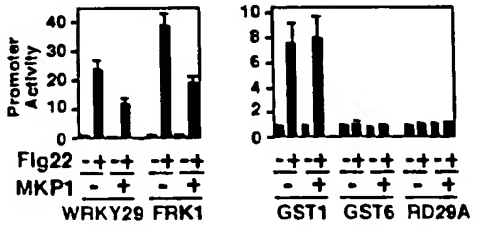
17 B



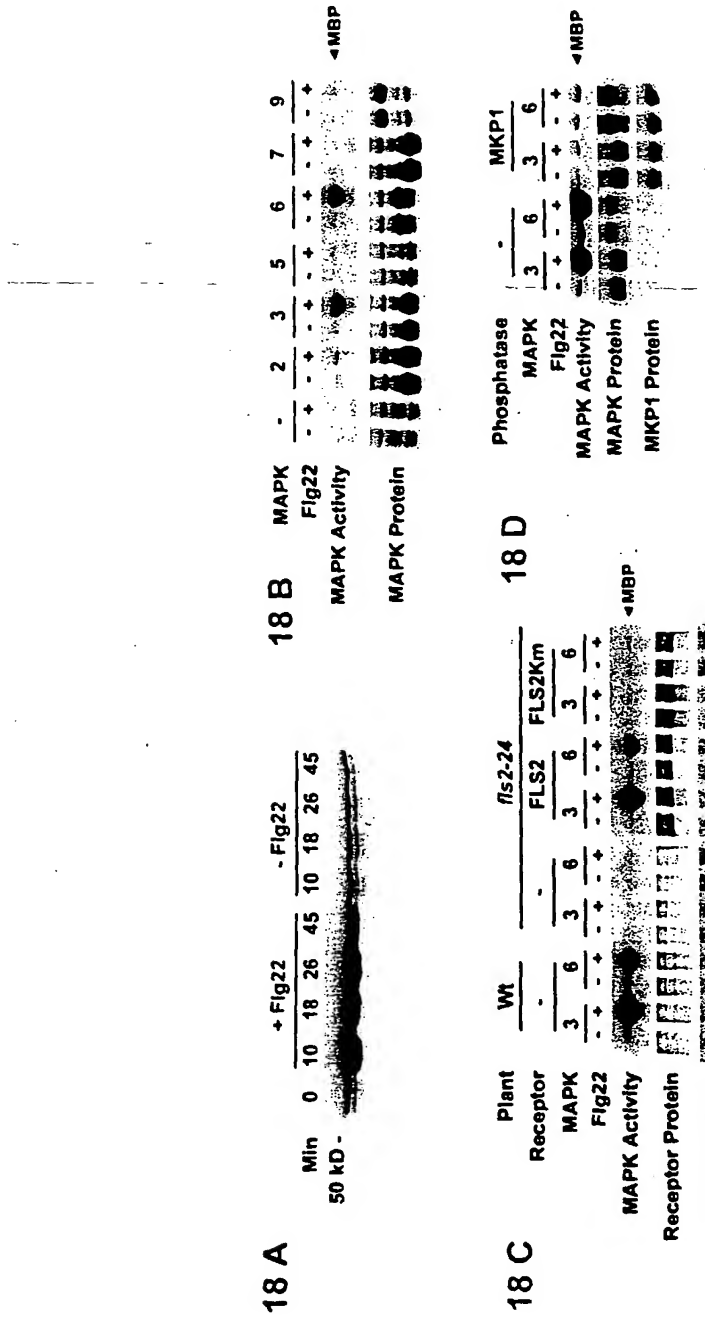
17 C



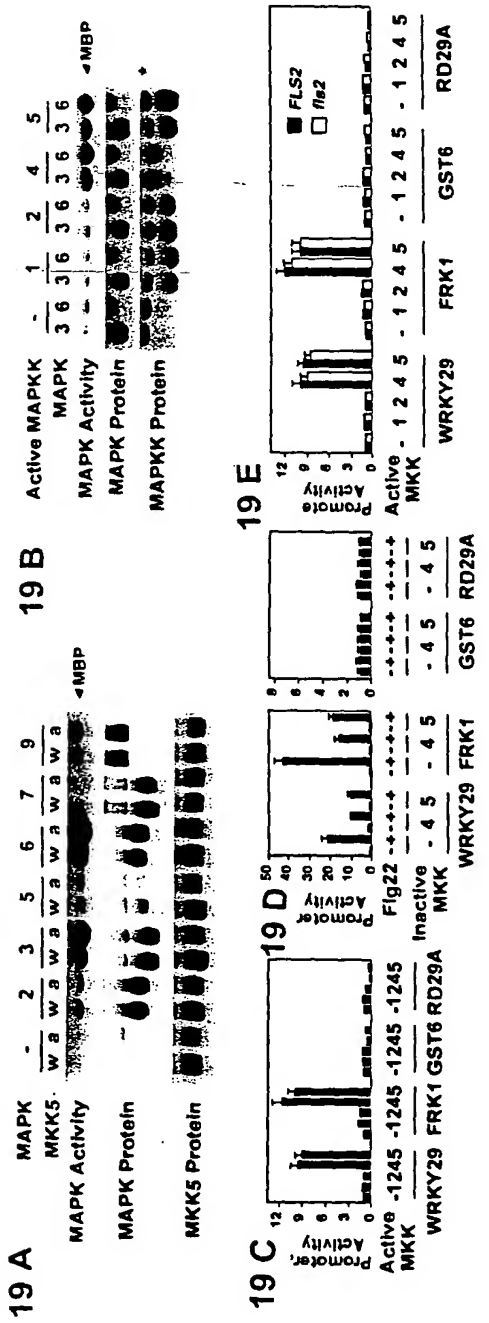
17 D



FIGURES 17 A-D

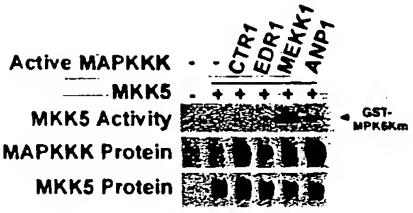


FIGURES 18 A-D

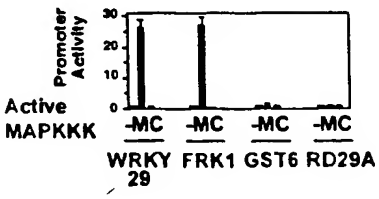


FIGURES 19 A-E

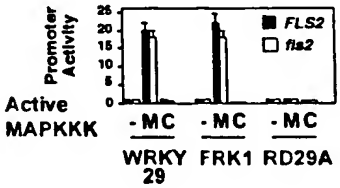
20 A



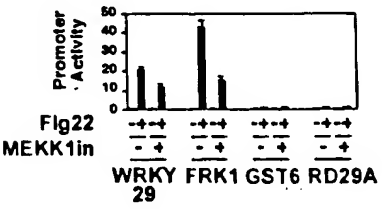
20 B



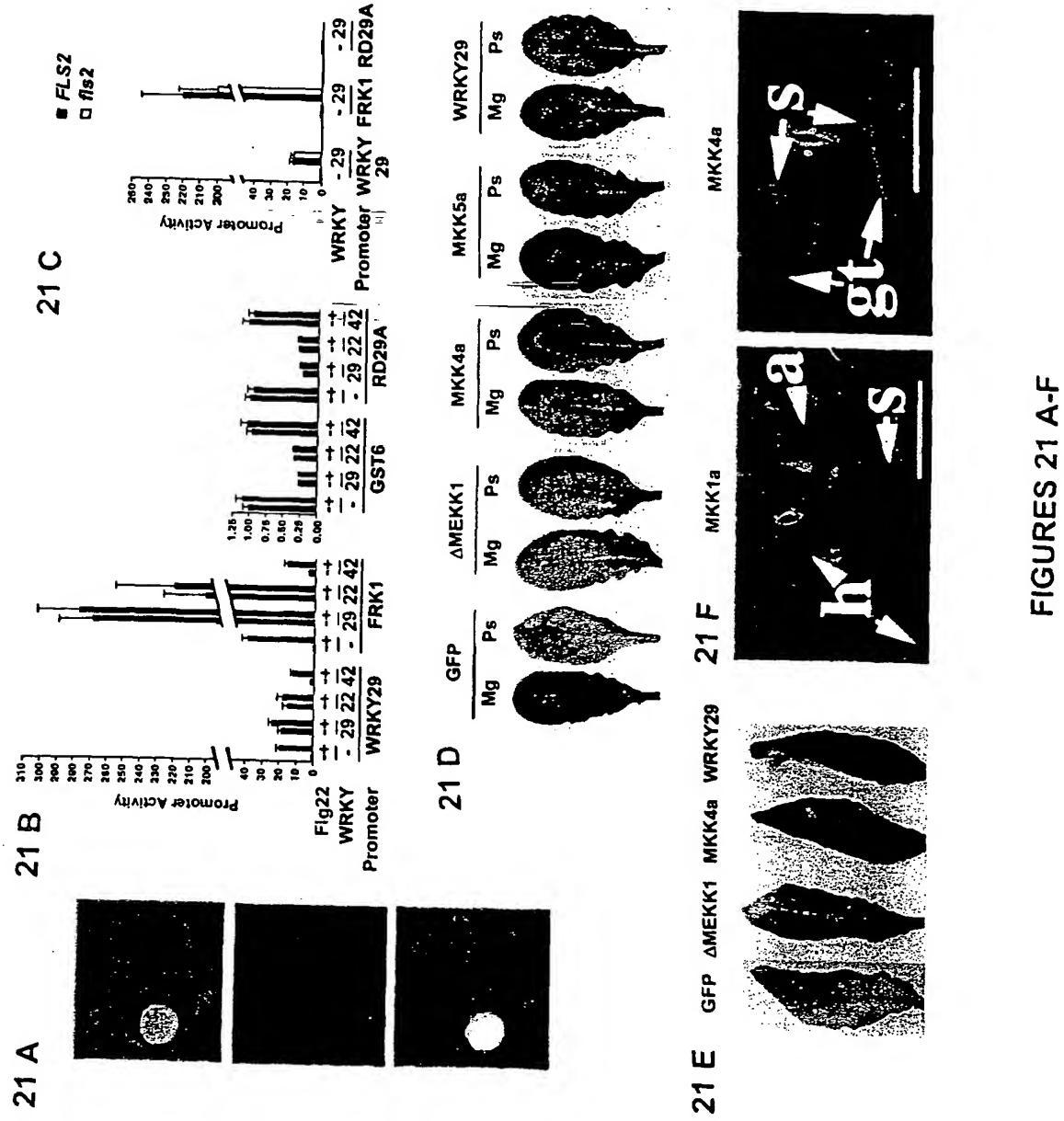
20 C



20 D



FIGURES 20 A-D



FIGURES 21 A-F

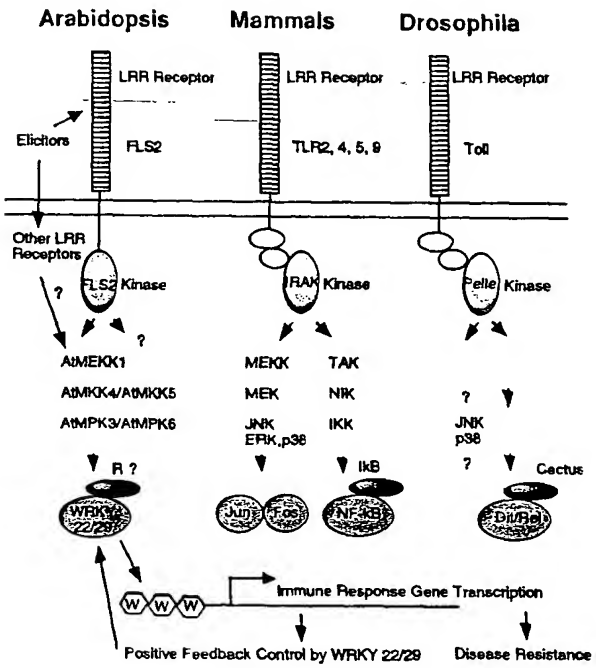

Arabidopsis
Mammals
Drosophila
LRR Receptor
LRR Receptor
LRR Receptor
Elicitors
FLS2
TLR2, 4, 5, 9
Toll
Other LRR Receptors
FLS2 Kinase
IRAK Kinase
Pelle Kinase
AtMEKK1
AtMKK4/AtMKK5
AtMPK3/AtMPK6
MEKK
MEK
JNK
EPK,p38
TAK
NIK
IKK
JNK
p38
R ?
IkB
Cactus
Jun
Fos
NF-κB
Dl/Rel
Immune Response Gene Transcription
Positive Feedback Control by WRKY 22/29
Disease Resistance

FIGURE 22